Biochemistry

DETERMINATION OF NEAREST NEIGHBOR EFFECTS ON THE CURRENT ASSIGNED RANDOM COIL VALUE OF ALANINE USING SOLID PHASE PEPTIDE SYNTHESIS

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Determination of the secondary structure of proteins has been indicated by comparison with the α-proton 'random coil' values of amino acids. Previously, it has been determined that chemical shift values upfield of the 'random coil' value will be an α-helix and downfield a β-sheet.[1] The 'random coil' value for the α-proton chemical shift of alanine was determined to be 4.35 ppm[2] without taking into account peptide length, pH conditions, denaturants (such as urea) or nearest neighbor amino acid effects. This study investigated the effect of the aromatic (phenylalanine, tyrosine and tryptophan) and aliphatic (leucine and valine) on the α-proton chemical shift of alanine. Pentapeptides were synthesized using solid phase peptide synthesis, purified using HPLC and analyzed using ^{1}H NMR according to the model Gly-Xaa-Ala-Yaa-Gly where Xaa and Yaa are any of the common amino acids (Figure 1). GFAFG, GLAFG, GFALG, GVAVG, GVALG, GLALG. GWAWG, GWALG, GFAYG, GYAYG, and GYALG have been successfully synthesized and purified. ^{1}H NMR studies have begun in order to determine the effect of the aromatic neighboring amino acids on the α-proton chemical shift of alanine. Preliminary results have demonstrated a significant difference from the currently assigned α-proton 'random coil' value for alanine with significant upfield shifts for neighboring aromatic residues.

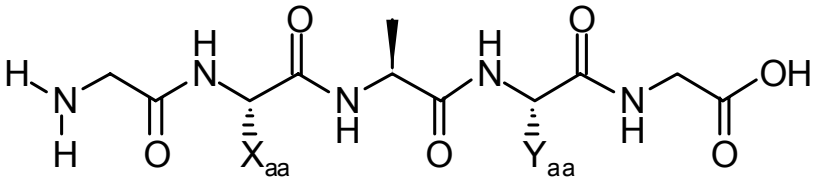

Figure 1. Model peptide with varying amino acids Xaa and Yaa.

[1] Wishart, D.S.; Sykes, B.D.; Richards, F.M. *J. Mol. Biol.* **1991**, *222,* 311-333.
[2] Bundi, A.; Wuthrich, K. *Biopolymers.* **1979**, *18,* 285-297.